Remarks/Arguments:

Claims 20-60, presented hereby, are pending.

Claim 1 is cancelled, hereby, without prejudice or disclaimer.

Claims 20 and 21 protect a nucleic acid sequence which consists in SEQ ID NO: 1, SEQ ID NO: 2 or fragments thereof or derived sequences therefrom. The claimed sequences that derive from SEQ ID NO: 1 or 2 enable specific detection of EHECs. The support for this amendment may be found in the specification, page 6, lines 30-35.

Reconsideration is requested in connection with the rejection of claim 1 under 35 USC 112, ¶1. Applicants submit that the replacement claims presented, hereby, render the rejection moot.

Reconsideration is requested with respect to the rejection of claim1 under 35 USC 112, ¶2, for reciting "high" stringency conditions.

Applicants consider the rejection poorly taken. One skilled in the art would readily construe this term as it is defined in the specification, page 7, lines 19-30, i.e., as referring to temperature and ionic strength conditions that allow specific hybridization between two complementary nucleic acid sequences, while limiting non-specific attachments.

Examples of such high stringency conditions are detailed in the specification. These may be:

- Hybridization, for instance at 37° C, with 5X SSPE, 0.5% Tween 20, 0.01% Merthiolate; washing with 10 mM Tris-HCl, 300 mM NaCl, 0.1% Tween 20, pH 7.4 (page 15, line 32-page 16, line 7),

- Hybridization in 6 x SSC, 5X Denhart's solution, 10% dextran sulphate, 10 mM EDTA, 0.5% SDS at 65° C; washing in 2X SSC at 65°C (page 18, lines 24-38).

Reconsideration is requested of the rejections of claim 1 under 35 USC 102(b) for alleged lack of novelty based on each of Brunder and Makino.

The invention defined in the new set of claims is both novel and unobvious over each of the cited references, as explained below.

The inventors demonstrated that *E. coli* O 157:7 are characterized by the stable integration of a portion of the IS 91 sequence into the kat P gene. Accordingly, the stable combination of a portion of IS 91 with a portion of kat P is a specific marker for *E. coli* O157:H7 strains (see page 5, lines 13 - page 6, line 17).

As shown in Figure 1, nucleotides spanning positions 1 to 406 of SEQ ID NO: 1 correspond to a portion of the IS 91 sequence; whereas, nucleotides 407 to 1499 correspond to a portion of the kat P gene (see, also, specification page 19, lines 36 - page 20, line 2).

The document Brunder et al. discloses the nucleotide sequence of the kat P gene. Accordingly, neither the whole sequence SEQ ID NO: 1, nor the oligonucleotide fragments, nor the sequences derived from SEQ ID NO: 1 that contains the IS 91/kat P junction from SEQ ID NO: 1, nor the primer pairs for amplification of a region of SEQ ID NO: 1 that span the IS 91/kat P junction (claim 6) is/are anticipated by Brunder et al.

Applicants, further, submit that one skilled in the art would have had no clue from reading Brunder et al. that a stable junction between the IS 91 sequence and kat P gene would be characteristic of *E. coli* O157:H7 strains.

As regards to Makino et al., attention is directed to specification page 3, line 34- page 4, line 5. The cited passages indicate that, while the plasmid pO157 isolated from an E. coli O157:H7 strain is discussed in Makino et al., the nucleotide sequence of this plasmid had not been made available to the public before the priority date of the present application.

Furthermore, the plasmid O157 isolated by Makino et al. was described as containing 1860 RFs. Isolation of this plasmid by Makino et al. does not amount to disclosing any of the 186 ORF contained therein. Thus. this plasmid does not inherently anticipate the claimed sequences, since the claims define a nucleic acid sequence consisting of SEQ ID NO: 1 or 2, or fragments or derived sequences thereof.

It appears that a word has been deleted in the English translation of the PCT (international) application (WO 99/55 908). The oligonucleotide sequences shown in the table spanning pages 12 and 13 of the present application are supposed to be derived from SEQ ID NOS: 1 and 2. However, according to the present specification, all listed sequences (SEQ ID NOS: 3 to 27) are positioned according to SEQ ID NO: 1.

SEQ ID NOS: 3 to 20 correspond to fragments of SEQ ID NO: 1; whereas, SEQ ID NOS: 21 to 27 correspond to fragments of SEQ ID NO: 2.

Accordingly, the term "SEQ ID NO: 2" should have been inserted between the lines "SEQ ID NO: 20: 395-412" and "SEQ ID NO: 21: 718-739".

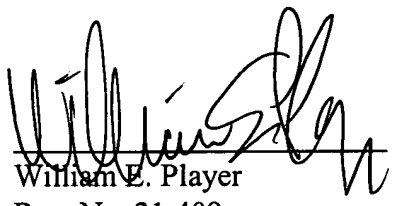
This term appeared in the table spanning pages 12-13 of the international patent application WO 99/55 908. A copy of these pages is enclosed.

However, should it not be possible to rely on the specification of the application WO 99/55 908, it should be easily drawn from the sequence listing that SEQ ID NO: 21-27 are fragments of SEQ ID NO: 2 rather than SEQ ID NO: 1.

Favorable action is requested.

Respectfully submitted,

JACOBSON HOLMAN PLLC

By 
William E. Player
Reg. No. 31,409

400 Seventh Street, NW
The Jenifer Building
Washington, D.C. 20004
Tel. (202) 638-6666
Fax (202) 393-5350
Date: May 12, 2004
WEP/bap
R:\rthomas\2004\APRIL\P66034US0.wpd